

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: US/10/57;552

Source: PST

Date Processed by STIC: 12-20-04

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 12/20/2004

PATENT APPLICATION: US/10/517,552

TIME: 15:05:44

Input Set : A:\B45310USSEQLIST.txt

Output Set: N:\CRF4\12202004\J517552.raw

4 <110> APPLICANT: CASSART, Jean-Pol  
5 GERARD, Catherine Marie Ghislaine  
6 PALMANTIER, Remi M.  
7 HAMBLIN, Paul A.  
9 <120> TITLE OF INVENTION: Immunogenic Compositions Comprising A Xenogenic Prostate Protein P501S  
11 <130> FILE REFERENCE: B45310  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/517,552  
C--> 15 <141> CURRENT FILING DATE: 2004-12-08  
15 <150> PRIOR APPLICATION NUMBER: PCT/EP03/06095  
16 <151> PRIOR FILING DATE: 2003-06-06  
18 <150> PRIOR APPLICATION NUMBER: GB 0213364.3  
19 <151> PRIOR FILING DATE: 2002-06-11  
21 <150> PRIOR APPLICATION NUMBER: GB 0221689.3  
22 <151> PRIOR FILING DATE: 2002-09-18  
24 <160> NUMBER OF SEQ ID NOS: 11  
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 553  
30 <212> TYPE: PRT  
31 <213> ORGANISM: Rattus norvegicus  
33 <400> SEQUENCE: 1  
34 Met Ile Gln Arg Leu Trp Ala Ser Arg Leu Leu Arg His Arg Lys Ala  
35 1 5 10 15  
36 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
37 20 25 30  
38 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
39 35 40 45  
40 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
41 50 55 60  
42 Leu Val Ser Val Pro Leu Leu Gly Ser Ala Ser Asp Gln Trp Arg Gly  
43 65 70 75 80  
44 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Val  
45 85 90 95  
46 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
47 100 105 110  
48 Leu Cys Ser Asp Thr Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
49 115 120 125  
50 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
51 130 135 140  
52 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
53 145 150 155 160  
54 Phe Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
55 165 170 175

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57          180          185          190
58 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
59          195          200          205
60 Ile Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Val Leu Gly
61          210          215          220
62 Pro Pro Glu Pro Ala Glu Gly Leu Leu Val Ser Ser Val Ser Arg Arg
63 225          230          235          240
64 Cys Cys Ser Cys His Ala Gly Leu Ala Phe Arg Asn Leu Gly Thr Leu
65          245          250          255
66 Phe Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
67          260          265          270
68 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
69          275          280          285
70 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
71          290          295          300
72 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
73 305          310          315          320
74 Ile Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
75          325          330          335
76 Phe Phe Ser Leu Val Met Asp Arg Leu Val Gln Lys Phe Gly Thr Arg
77          340          345          350
78 Ser Val Tyr Leu Ala Ser Val Met Thr Phe Pro Val Ala Ala Ala Ala
79          355          360          365
80 Thr Cys Leu Ser His Ser Val Val Val Thr Ala Ser Ala Ala Leu
81          370          375          380
82 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
83 385          390          395          400
84 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
85          405          410          415
86 Asp Ala Gly Gly Gly Ser Ser Glu Asp Ser Gln Thr Thr Ser Phe Leu
87          420          425          430
88 Leu Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Pro
89          435          440          445
90 Gly Gly Ser Ser Ile Leu Val Pro Pro Pro Ala Leu Cys Gly Ala Ser
91          450          455          460
92 Ala Cys Asp Val Ser Met Arg Val Val Val Gly Glu Pro Pro Glu Ala
93 465          470          475          480
94 Lys Val Val Thr Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
95          485          490          495
96 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
97          500          505          510
98 Ile Val Gln Leu Ser His Ser Val Thr Ala Tyr Met Val Ser Ala Ala
99          515          520          525
100 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
101          530          535          540
102 Lys Asn Asp Leu Ala Lys Tyr Ser Leu
103 545          550
106 <210> SEQ ID NO: 2

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Input Set : A:\B45310USSEQLIST.txt

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107 &lt;211&gt; LENGTH: 2314

108 &lt;212&gt; TYPE: DNA

109 &lt;213&gt; ORGANISM: Rattus norvegicus

111 &lt;400&gt; SEQUENCE: 2

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113 ttcacacatt tcgagcttta gttccgatcc ccagaacatc cacgtagttt ttctggcctt 120
114 ctggctgagc catggaggcc gacagaggag gggagaagtt tgaagcttga gaaggatttc 180
115 cgtatgcgca aggtaccca tgcttgctt tctcccatg accctggtca gccctcctct 240
116 gccctcctct tctgcccc cttctctcca gggctcgact gacgagatgt gtccccatca 300
117 agcaaggcac tagatggtga cgtgttcagt gtgggatgag atgccgaagt ggtactcaag 360
118 ggctggccga aatgggagcc tggctgcacc ctccggaggt ggtgctagca aggaggagaa 420
119 gccgcggcag ggctgactca aaacagctgt ggggtgtgtg aatggcccc ggaccctaa 480
120 ccgccctgtc catcatgata cagaggctgt gggccagccg tctgctaagg catcgaaaag 540
121 ccagctcct gctgggtcaac ctgctaacct tcggcctgga ggtgtgcctg gctgctggca 600
122 ttacctatgt gccaccctt ctgctggaag tcggggtaga ggaaaagt atgaccatgg 660
123 tgttgggcat tggccagtgt ctgggcctgg tttctgttcc actcctaggc tcagccagtgt 720
124 accagtggcg tgggcgtat ggccgcgga gaccctttat ctgggctctg tccctgggtg 780
125 tctgctaag cctcttctc atcccgagg ccggctggct ggcagggcta ctgtgttcag 840
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127 gccagggtgt ctttactcca ctggaggcct tactctccga cctcttccg gaccagacc 960
128 actgccgcca agccttctct gtctatgcct tcatgatcag cctcgggggc tgccctgggt 1020
129 acctcttacc tgccattgac tgggacacca gcgccctggc cccctaccta ggcactcagg 1080
130 aagaatgcct ctccggcctc ctccacctca tttttctcat ctgtgtggca gccactctgc 1140
131 ttgtggctga ggaggcagtc cttggcccac ccgagccagc agaagggttg ttggtctcct 1200
132 ccgtgtcacg ccggtgctgc tcatgccatg ctggcctggc tttccggaat ctgggtaccc 1260
133 tgtttccccg gctgcaccag ctgtgctgcc gaatgcctcg caccctgcgc cggctctttg 1320
134 tggctgagct gtgcagctgg atggcactta tgactttcac actgttctac acggacttgc 1380
135 tgggagaggg gctgtaccag ggtgtcccca gacagagcc aggtaccgag gcccgagac 1440
136 actatgatga aggcattcga atgggcagcc tggggctctt cctgcagtgt gccatctccc 1500
137 tgttcttctc cctggtcagt gacaggctgg tacagaagtt cggcacacgg tcagtctacc 1560
138 tggccagtgt gatgacctt cccgtggctg ccgctgccac gtgcctgtcc cacagcgtgg 1620
139 ttgtagtac agcctcagct gccctacccg ggttcacct ctcagccttg cagatcctgc 1680
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141 gggacgctgg aggtggtagc agtgaagaca gccaaacaac cagcttcttg ctaggcccta 1800
142 agccaggagc tcccttcccc aatggacacg tgggccctgg ccgacagcag atcctggtgc 1860
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147 actttgttac acaggtagtg tttgacaaga atgacttggc caaatactca ctgtagaatt 2160
148 ctgtaaggca tcaaagaaga ggatctgcct ccccggttct cagccccaga gggctgcaga 2220
149 gctggtctct ttccggtctc tgttgccctg agtggctctc cactgccatc cgaaggcagt 2280
150 gaggtgtatg gctgcacagg ttggagcttt tggc                                     2314

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152 &lt;210&gt; SEQ ID NO: 3

153 &lt;211&gt; LENGTH: 553

154 &lt;212&gt; TYPE: PRT

155 &lt;213&gt; ORGANISM: Maccaca fascicularis

157 &lt;400&gt; SEQUENCE: 3

158 Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala

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159 1          5          10          15
160 Gln Leu Leu Leu Ile Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
161          20          25          30
162 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
163          35          40          45
164 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
165          50          55          60
166 Leu Val Ser Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
167 65          70          75          80
168 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
169          85          90          95
170 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
171          100         105         110
172 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
173          115         120         125
174 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
175          130         135         140
176 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
177 145          150         155         160
178 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
179          165         170         175
180 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
181          180         185         190
182 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
183          195         200         205
184 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
185          210         215         220
186 Pro Ala Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Pro Ser His
187 225          230         235         240
188 Cys Cys Pro Cys Trp Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
189          245         250         255
190 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
191          260         265         270
192 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
193          275         280         285
194 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
195          290         295         300
196 Pro Arg Ala Glu Leu Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
197 305          310         315         320
198 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
199          325         330         335
200 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
201          340         345         350
202 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
203          355         360         365
204 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
205          370         375         380
206 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
207 385          390         395         400

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208 Ser Leu Tyr His Arg Glu Arg Gln Val Phe Leu Pro Lys Tyr Arg Gly
209                               405                               410                               415
210 Asp Ala Gly Gly Thr Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
211                               420                               425                               430
212 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
213                               435                               440                               445
214 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
215                               450                               455                               460
216 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
217 465                               470                               475                               480
218 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
219                               485                               490                               495
220 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
221                               500                               505                               510
222 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
223                               515                               520                               525
224 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
225                               530                               535                               540
226 Lys Ser Asp Leu Ala Lys Tyr Ser Val
227 545                               550

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230 &lt;210&gt; SEQ ID NO: 4

231 &lt;211&gt; LENGTH: 3514

232 &lt;212&gt; TYPE: DNA

233 &lt;213&gt; ORGANISM: Maccaca fascicularis

235 &lt;400&gt; SEQUENCE: 4

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236 aaaaaaaaaag ccgcccgttg gcgcgcgttg ggggcaagga aaagaggggg gaaaccagtc 60
237 tgcacgcgct ggctccgggt gacagccgcg cgcctaggcc aggcagcgct tccctctgtc 120
238 acccagactg gaggcaatgt tctgatcact gcacactgca cccttgacct ccagactca 180
239 agcaatcctc ccattctcagc ctcttaagta gctgggacca caggatctga gtgatgagat 240
240 gtgtcccccac tgagggtgccc cacagcagca ggtgttgagc atgggctgag aagctggacc 300
241 ggcaccaaag ggctggcgga aatgggcgcc tggctgattc ctaggcagtt ggccgagca 360
242 agggaggagag gccgtggcctt ccggagcaga gcggagacga agcagttctg gagtgcctaa 420
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253 ccctacctgg gcacccagga ggagtgcctc tttggcctgc tcaccctcat ctccctcacc 1080
254 tgcgtagcag ccacactgct ggtggccgag gaggcagcac tgggccccgc cgagccagcg 1140
255 gaagggtctt ttgccccctc cctgccgtcc cactgctgtc cgtgctgggc ccgcctggct 1200
256 ttccggaacc tgggcgcctt gcttccccgc ctgcaccagc tgtgctgccg catgccccgc 1260
257 accctgcgcc ggctctctgt ggctgagctg tgcagctgga tggcactcat gaccttcacg 1320
258 ctgttttaca cggatttcgt gggcgagggg ctataccagg gcgtgcccag agctgagctg 1380
259 ggcaccgagg cccggagaca ctatgatgaa ggcgttcgga tgggcagttc ggggctgttc 1440

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VERIFICATION SUMMARY

DATE: 12/20/2004

PATENT APPLICATION: US/10/517,552

TIME: 15:05:45

Input Set : A:\B45310USSEQLIST.txt

Output Set: N:\CRF4\12202004\J517552.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date